Comparison of sheep genotype metrics across breeds and countries

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The objective of the present study was to compare the allele frequency of different meat sheep breeds in Ireland and the United Kingdom as well as different dairy sheep breeds from France. The frequency of each allele per single nucleotide polymorphism (SNP) was available for five meat sheep breeds from Ireland (i.e. Belclare, Charollais, Suffolk, Texel and Vendeen), two meat sheep breeds from the UK (i.e. Scottish Blackface and Texel), and five French dairy sheep breeds (i.e. Basco-Béarnaise, Black-faced Manech, Corse, Lacaune, and Red-faced Manech). Allele frequency data were available on 44,040, 577,400 and 48,059 SNPs from the sheep in Ireland, the UK, and France, respectively. A total of 38,883 SNPs were common to all sheep populations. All genotyping had been undertaken using Illumina platforms and the allele frequencies of all SNPs were subsequently aligned to the Illumina 'Allele A/B' format; the frequency of the 'A' allele was subsequently calculated in each of the 12 populations. An informative SNP was identified where the frequency of the 'A' allele was between 0.2 and ≤0.8 in each of two pair-wise breeds compared. A non-informative SNP was defined as when the two breeds were compared, the frequency of the 'A' allele in either breed was either <0.2 or >0.8. On average, 49.33% of all 38,883 common SNPs were informative between each of the 66 pairwise comparisons. The pair of breeds with the maximum number of informative SNPs was, as expected, the Irish Texel and Scottish Texel (59.89% of SNPs were informative) breeds; the minimum number of informative SNPs between the Scottish Texel and Irish Suffolk (40.49% of SNPs). The number of SNPs that were informative in one breed but non-informative in another ranged from 1,081 (informative in the Scottish Texel but not in the Irish Texel breed) to 9,350 (informative in the Corse but not in the Suffolk breed). The present study identified both informative and non-informative SNPs across both meat and dairy sheep. The results from the present study will contribute to the development of future genotyping panels for sheep to maximise the applicability of the genotyping panel across multiple sheep populations.

Study of rumen microbiota in dairy sheep with different feed efficiency using nanopore sequencing

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Ruminants can obtain high-quality products using low-quality forages, which are mainly indigestible for humans. Until now, second-generation massive parallel sequencing has been the most used technology in the majority of studies of microbiota in livestock species using two approaches; 16S rRNA gene sequencing and shotgun metagenomics. However, the launching of third-generation single-molecule technologies offers long-read output with low cost and rapid real-time analysis. In this preliminary study, we aim to assess the complete end-to-end microbial composition of rumen using the MinION sequencer (Oxford Nanopore Technology) in two groups of ewes with divergent residual feed intake (RFI) values. From a total of 40 lactating Assaf ewes, the 20% most efficient (RFI<-0.40) and inefficient (RFI>0.39) sheep were selected for DNA sequencing of ruminal fluid, using Nanopore technology. The fluid was collected with a stomach tube. After quality control and removing host DNA, an average of 380.000 reads per sample with a mean length of 714 bases were aligned against the NCBI-nr protein database performing taxonomic and functional assignments on individual reads rather than contigs. No significant differences were detected in the microbial community between the feed efficiency groups studied here. Predominant genera among samples were *Prevotella*, *Methanobrevibacter* and *Fibrobacter*, as usually found in other rumen studies. Also, some of the functions observed in this research, such as methane metabolism, peptidoglycan biosynthesis, energy production and conversion, protein degradation and inorganic ion transport, could be related with higher feed efficiency in dairy ewes. These preliminary results suggest a more relevant role of microbiota function than taxonomy in explaining differences in feed efficiency in dairy sheep. Projects: EU-SMARTER & JCyL CSI276P18, FEDER and ESF.

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